Does ~~~ ~~~ply
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/975,719

DATE: 03/14/2002
TIME: 12:16:59

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\03142002\I975719.raw**

```
 4 <110> APPLICANT: Ausubel, Frederick M.
 5         Rahme, Laurence G.
 7 <120> TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
 8         SEQUENCES AND USES THEREOF
10 <130> FILE REFERENCE: 00786/361003
12 <140> CURRENT APPLICATION NUMBER: US 09/975,719
13 <141> CURRENT FILING DATE: 2001-10-10
15 <150> PRIOR APPLICATION NUMBER: US 09/199,637
16 <151> PRIOR FILING DATE: 1998-11-25
18 <150> PRIOR APPLICATION NUMBER: US 60/066,517
19 <151> PRIOR FILING DATE: 1997-11-25
21 <160> NUMBER OF SEQ ID NOS: 437
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
1045 <210> SEQ ID NO: 13
1046 <211> LENGTH: 1046
1047 <212> TYPE: PRT
1048 <213> ORGANISM: Pseudomonas aeruginosa
1050 <400> SEQUENCE: 13
1051 Pro Gly Arg Leu His Pro His Gly Gln Gln Arg Asp Pro Gln Ser Val
1052  1               5                  10                  15
1053 Gln Thr Thr Ala Gln Ser Arg Pro Gly Asp Val Cys Val Pro Ala Pro
1054                 20                  25                  30
1055 Gly Arg Gln Arg Ser Arg Pro Gly Thr Gly Leu His His Arg Val Pro
1056             35                  40                  45
1057 Leu Leu Pro Ala Ser Pro Val Arg His Ala Gly Arg Thr His Gly Gly
1058      50                  55                  60
1059 Leu Leu Met Gly Phe Phe Gln Thr Leu Leu Arg Gly Arg Thr Gln Pro
1060 65                  70                  75                  80
1061 Gln Ser Val Pro Ala Asp Ala Pro Glu Asp Ser Gly Ala Leu Asp Val
1062                 85                  90                  95
1063 Ala Ala Ala Glu Glu Ala Thr Glu Arg Tyr Leu Ala Arg Leu Ala Ala
1064                 100                 105                 110
1065 Met Gly Ile Pro Leu Pro Asn Thr Gly Ser Lys Asn Gly Ala Thr Gln
1066             115                 120                 125
1067 Ala Glu Ala Ser Arg Leu Tyr Asp His Asp Pro Ser Phe Val Asp Leu
1068      130                 135                 140
1069 Leu Pro Trp Ala Glu Tyr Leu Pro Asp Glu Gln Val Met Leu Leu Glu
1070 145                 150                 155                 160
1071 Asp Gly Arg Ser Arg Ala Ala Phe Phe Glu Leu Val Pro Leu Gly Thr
```

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\03142002\I975719.raw

```
1072                 165                 170                 175
1073 Glu Gly Arg Asp Pro Asn Trp Met Gln Asn Ala Arg Asp Ala Leu Lys
1074             180                 185                 190
1075 Glu Ala Leu Gln Asn Ser Phe Asp Glu His Glu Thr Ser Pro Trp Ile
1076         195                 200                 205
1077 Val Gln Phe Tyr Ala Gln Asp Glu Ile Ser Trp Asp Asn Phe Gln Glu
1078     210                 215                 220
1079 Gln Leu Arg Gln Tyr Val His Pro Arg Ala Arg Gly Ser Ala Phe Ser
1080 225                 230                 235                 240
1081 Glu Met Tyr Leu Ala Leu Met Lys His His Leu Glu Gly Ile Ser Lys
1082             245                 250                 255
1083 Pro Gly Gly Leu Phe Val Asp Thr Ala Val Ser Lys Leu Pro Trp Arg
1084             260                 265                 270
1085 Gly Gln Gln Arg Arg Val Arg Met Val Val Tyr Arg Arg Ile Arg Lys
1086         275                 280                 285
1087 Glu Asp Ala Gln Ile Arg Gly Gln Asp Pro Ala Ala Tyr Leu Lys Ser
1088     290                 295                 300
1089 Ile Cys Glu Arg Ile Gln Gly Gly Leu Ala Asn Ala Gly Ile Val Ala
1090 305                 310                 315                 320
1091 Ser Arg Met Gly Gly Gln Glu Ile Arg Asn Trp Leu Ile Arg Trp Phe
1092             325                 330                 335
1093 Asn Pro His Pro Asp His Leu Gly Gln Ala Glu Ala Asp Leu Arg Arg
1094             340                 345                 350
1095 Phe Tyr Glu Leu Val Cys Arg Pro Asp Glu Pro Ile Leu Gln Asp Glu
1096         355                 360                 365
1097 Leu Pro Leu Ala Asp Gly Thr Asp Phe Ser Gln Asn Leu Phe Tyr Arg
1098     370                 375                 380
1099 Gln Pro Val Ser Asp Ala Thr Gln Gly Val Trp Leu Phe Asp Ala Met
1100 385                 390                 395                 400
1101 Pro His Arg Val Ile Val Val Asp Gln Leu Asn Lys Ala Pro Leu Thr
1102             405                 410                 415
1103 Gly His Phe Thr Gly Glu Thr Leu Lys Gly Asp Gly Leu Asn Ala Leu
1104             420                 425                 430
1105 Phe Asp Arg Met Pro Glu Asp Thr Leu Leu Cys Ile Thr Met Val Val
1106         435                 440                 445
1107 Thr Pro Gln Asp Met Leu Glu Gly His Leu Gln Gln Leu Ser Lys Lys
1108     450                 455                 460
1109 Ala Val Gly Asp Thr Gln Ala Ser Ile His Thr Arg Glu Asp Val Ala
1110 465                 470                 475                 480
1111 Thr Val Arg Arg Leu Ile Gly Arg Glu His Lys Leu Tyr Arg Gly Ala
1112             485                 490                 495
1113 Ile Ala Leu Phe Val Arg Gly Arg Asp His Thr Gln Leu Glu Glu Arg
1114         500                 505                 510
1115 Cys Ile Thr Leu Ser Asn Val Leu Leu Gly Ala Gly Leu Val Pro Val
1116         515                 520                 525
1117 Glu Pro Gln Asn Glu Val Gly Pro Leu Asn Ser Tyr Leu Arg Trp Leu
1118     530                 535                 540
1119 Pro Ser Asn Phe Asp Pro Asn Glu Lys Arg Ala Leu Glu Trp Tyr Thr
1120 545                 550                 555                 560
```

RAW SEQUENCE LISTING   DATE: 03/14/2002
PATENT APPLICATION: US/09/975,719   TIME: 12:16:59

Input Set : A:\PTO.VSK.txt
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```
1121 Gln Met Met Phe Ala Gln His Ile Ala Asn Leu Ser Pro Ile Trp Gly
1122             565                 570                 575
1123 Arg Thr Thr Gly Thr Gly His Pro Gly Phe Thr Leu Phe Asn Arg Gly
1124             580                 585                 590
1125 Gly Ala Pro Leu Thr Phe Asp Pro Phe Asn Lys Leu Asp Arg Gln Met
1126             595                 600                 605
1127 Asn Ala His Gly Phe Ile Phe Gly Pro Thr Gly Ser Gly Lys Ser Ala
1128     610                 615                 620
1129 Ser Leu Thr Asn Leu Ile Cys Gln Met Leu Ala Met Tyr Leu Pro Arg
1130 625                 630                 635                 640
1131 Met Phe Val Ala Glu Ala Gly Asn Ser Phe Gly Leu Leu Ala Asp Leu
1132             645                 650                 655
1133 Ala Lys Arg Phe Gly Leu Ser Val His Arg Val Arg Leu Ala Pro Gly
1134             660                 665                 670
1135 Ser Gly Val Ser Leu Ala Pro Phe Ala Asp Ala Ile Lys Leu Val Glu
1136             675                 680                 685
1137 Ser Pro Asp Gln Val Lys Val Leu Asp Ala Glu Asp Ile Glu Ala Ser
1138     690                 695                 700
1139 Asp Ser Val Gln Gly Ser Lys Ala Asp Leu Glu Asp Asp Gln Arg Asp
1140 705                 710                 715                 720
1141 Ile Leu Gly Glu Met Glu Ile Val Ala Arg Leu Met Ile Thr Gly Gly
1142             725                 730                 735
1143 Glu Glu Lys Glu Asp Ala Arg Leu Thr Arg Ala Asp Arg Ser Ala Val
1144             740                 745                 750
1145 Arg Gln Ala Ile Leu Ala Ala Ala Arg Thr Cys Ala Ala Ala Asn Arg
1146             755                 760                 765
1147 Thr Val Leu Thr Gln Asp Val Arg Asp Ala Leu Tyr Glu Ala Ser Arg
1148     770                 775                 780
1149 Ser Asp Ser Thr Ala Pro Glu Arg Arg Ala Arg Ile Ala Glu Met Ala
1150 785                 790                 795                 800
1151 Glu Ala Met Gln Met Phe Cys Met Gly Ala Asp Gly Glu Met Phe Asn
1152             805                 810                 815
1153 Arg Glu Gly Thr Pro Trp Pro Glu Ala Asp Leu Thr Val Val Asp Phe
1154             820                 825                 830
1155 Ala Thr Tyr Ala Arg Glu Gly Tyr Ala Ala Gln Leu Gly Ile Ala Tyr
1156             835                 840                 845
1157 Ile Ser Leu Leu Asn Thr Val Asn Asn Ile Ala Glu Arg Asp Gln Phe
1158     850                 855                 860
1159 Lys Gly Arg Pro Ile Val Lys Ile Thr Asp Glu Gly His Ile Ile Thr
1160 865                 870                 875                 880
1161 Lys His Pro Leu Leu Leu Pro Tyr Ala Met Lys Ile Thr Lys Met Trp
1162             885                 890                 895
1163 Arg Lys Leu Gly Ala Trp Phe Trp Leu Ala Thr Gln Asn Ile Asp Asp
1164             900                 905                 910
1165 Ile Pro Ala Ser Gly Ala Pro Met Leu Asn Met Ile Glu Trp Trp Leu
1166             915                 920                 925
1167 Cys Leu Asn Met Pro Pro Asp Glu Val Glu Lys Ile Ser Arg Phe Arg
1168     930                 935                 940
1169 Glu Leu Ser Pro Ala Gln Lys Ser Met Met Leu Ser Ala Arg Lys Glu
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/975,719

DATE: 03/14/2002
TIME: 12:16:59

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\03142002\I975719.raw

```
1170 945                  950              955                960
1171 Ser Gly Lys Phe Thr Glu Gly Val Leu Leu Ala Lys Gly Lys Glu Tyr
1172                  965              970              975
1173 Leu Val Arg Val Val Pro Pro Ser Leu Tyr Leu Ala Leu Ala Met Thr
1174                  980              985              990
1175 Glu Asn Glu Glu Lys Asn Gln Arg Tyr Asn Ile Met Gln Ala Thr Gly
1176            995              1000            1005
1177 Cys Asp Glu Leu Glu Ala Ala Leu Gln Val Ala Ala Asp Leu Asp Lys
1178      1010            1015            1020
1179 Ala Arg Gly Leu Pro Pro Phe Pro Ile Val Phe Pro Asp Gln Pro Ala
E--> 1180 1025            1030            1035
1181 Val Glu Cys Gln Asp Glu
1182                  1045
```

(104) — should be 1040

```
12264 <210> SEQ ID NO: 405
12265 <211> LENGTH: 1198
12266 <212> TYPE: PRT
12267 <213> ORGANISM: Pseudomonas aeruginosa
12269 <400> SEQUENCE: 405
12270 Cys Ala Gly Ser Ala Arg Ser Thr Thr Lys Pro Thr Ala Ala Pro Ser
12271 1               5                10               15
12272 Thr Arg Arg Ala Glu Arg Leu Phe Tyr Arg Pro Phe Met His Ala Cys
12273            20               25               30
12274 Ile Pro Thr Asp Trp Ser Gln Arg Met Ile His Gln Ile Thr Arg Ala
12275      35               40               45
12276 Gly Lys Ser Leu Leu Ala Ala Gly Cys Thr Leu Ser Ile Leu Phe Ala
12277      50               55               60
12278 Ser Asp Ser Tyr Ala Ala Thr Ala Leu Asn Val Ser Gln Gln Pro Leu
12279 65               70               75               80
12280 Phe Leu Thr Gln Gly Val Ala Pro Asn Leu Leu Phe Thr Leu Asp Asp
12281                  85               90               95
12282 Ser Gly Ser Met Ala Trp Ala Tyr Val Pro Asp Gly Ile Ser Gly Asn
12283                  100              105              110
12284 Ser Gly Arg Ala Gly Arg Ser Ser Asp Tyr Asn Ala Leu Tyr Tyr Asn
12285            115              120              125
12286 Pro Asp Tyr Ala Tyr Gln Val Pro Lys Lys Leu Thr Leu Ser Gly Asp
12287      130              135              140
12288 Gln Ile Ile Val Ser Asp Tyr Pro Val Pro Arg Phe Thr Ala Ala Trp
12289 145              150              155              160
12290 Gln Asp Gly Tyr Ala Gln Gly Ser Thr Thr Asn Leu Ser Asn Asn Tyr
12291                  165              170              175
12292 Arg Pro Gln Trp Gly Thr Gly Trp Leu Gly Cys Ile Asp Ser Ser Cys
12293            180              185              190
12294 Asn Thr Gly Arg Ala Tyr Tyr Tyr Thr Tyr Lys Val Ser Ala Ser Cys
12295            195              200              205
12296 Pro Ala Gln Pro Val Ser Ser Ser Asn Ser Cys Tyr Thr Tyr Asn Ala
12297      210              215              220
12298 Leu Pro Thr Ser Gln Glu Ser Asn Phe Ala Ile Trp Tyr Ser Tyr Tyr
12299 225              230              235              240
12300 Arg Asn Arg Ile Leu Ala Thr Lys Thr Ala Ala Asn Leu Ala Phe Tyr
```

```
12301                245              250              255
12302 Ser Leu Pro Glu Asn Val Arg Leu Thr Trp Gly Ala Leu Asn Thr Cys
12303                260              265              270
12304 Ser Ile Gly Ala Asn Ser Arg Ser Cys Gln Asn Asn Ala Leu Leu Gln
12305                275              280              285
12306 Phe Asn Lys Gln His Lys Ile Asn Phe Phe Asn Trp Leu Ala Asn Ser
12307          290              295              300
12308 Pro Ala Ser Gly Gly Thr Pro Leu His Ala Ala Leu Asp Arg Ala Gly
12309 305              310              315              320
12310 Arg Phe Leu Gln Thr Asn Gly Thr Ala Tyr Thr Thr Glu Asp Gly Lys
12311                325              330              335
12312 Thr Tyr Ser Cys Arg Ala Ser Tyr His Ile Met Met Thr Asp Gly Ile
12313                340              345              350
12314 Trp Asn Gly Arg Asn Val Thr Pro Gly Asn Leu Asp Asn Gln Asn Gln
12315                355              360              365
12316 Thr Phe Pro Asp Ser Thr Leu Tyr Arg Pro Gln Pro Pro Tyr Ala Asp
12317          370              375              380
12318 Ser Asn Ala Ser Ser Leu Ala Asp Leu Ala Phe Lys Tyr Trp Thr Thr
12319 385              390              395              400
12320 Asp Leu Arg Pro Ser Ile Asp Asn Asp Leu Lys Pro Phe Met Ala Tyr
12321                405              410              415
12322 Lys Ser Gly Asp Asp Ser Lys Asp Tyr Trp Asp Pro Arg Asn Asn Pro
12323                420              425              430
12324 Ala Thr Trp Gln His Met Val Asn Phe Thr Val Gly Leu Gly Leu Ser
12325                435              440              445
12326 Tyr Ser Leu Thr Leu Asn Ser Ala Pro Thr Trp Thr Gly Ser Thr Phe
12327          450              455              460
12328 Gly Asn Tyr Glu Glu Leu Met Ala Gly Ser Lys Ala Trp Pro Ser Val
12329 465              470              475              480
12330 Asp Asn Asp Ala Ala Pro Gly Asn Val Tyr Asp Leu Trp His Ala Ala
12331                485              490              495
12332 Ile Asn Ser Arg Gly Asp Phe Phe Ser Ala Glu Ser Pro Asp Ser Leu
12333                500              505              510
12334 Val Gln Ala Phe Asn Lys Ile Leu Thr Arg Ile Ser Glu Arg Asn Thr
12335                515              520              525
12336 Ser Ser Ser Lys Pro Ala Met Thr Ser Ala Leu Gln Asp Asp Gly Thr
12337          530              535              540
12338 Gly Asp Lys Leu Ile Arg Tyr Ser Tyr Gln Ser Ser Phe Ala Ser Asp
12339 545              550              555              560
12340 Lys Asn Trp Ala Gly Asp Leu Ile Arg Tyr Lys Val Glu Ser Thr Ser
12341                565              570              575
12342 Thr Gly Ser Thr Lys Thr Gln Glu Trp Ser Ala Gly Ala Leu Leu Asp
12343                580              585              590
12344 Asn Arg Ala Pro Ala Thr Arg Asn Ile Tyr Ile Ala Ser Asn Ser Gly
12345                595              600              605
12346 Thr Asn Arg Leu Lys Pro Phe Thr Trp Ser Asn Ile Glu Gly Ser Gln
12347          610              615              620
12348 Leu Ala Thr Trp Leu Asn Arg Asn Pro Asp Lys Asp Asn Gln Ala Asp
12349 625              630              635              640
```

RAW SEQUENCE LISTING   DATE: 03/14/2002
PATENT APPLICATION: US/09/975,719   TIME: 12:17:02

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\03142002\I975719.raw

```
12350 Thr Lys Gly Ala Gln Arg Val Asp Phe Ile Arg Gly Gln Gln Asn Met
12351             645                 650                 655
12352 Asp Gly Phe Arg Gln Arg Gln Ala Val Leu Gly Asp Ile Val His Ser
12353             660                 665                 670
12354 Ser Pro Ala Val Val Gly Pro Ala Gln Tyr Leu Thr Tyr Leu Ala Asn
12355             675                 680                 685
12356 Pro Ile Glu Pro Ser Gly Asp Tyr Gly Thr Phe Lys Thr Glu Ala Asp
12357         690                 695                 700
12358 Gln Arg Ser Pro Arg Val Tyr Val Gly Ser Asn Asp Gly Met Leu His
12359 705                 710                 715                 720
12360 Gly Phe Asn Ile Lys Thr Gly Val Glu Glu Phe Ala Phe Ile Pro Thr
12361             725                 730                 735
12362 Ala Val Phe Glu Lys Leu Asn Lys Leu Thr Gly Ile Ser Tyr Gln Gly
12363             740                 745                 750
12364 Gly Ala His Gln Tyr Phe Val Asp Ala Thr Pro Val Val Ser Asp Ala
12365             755                 760                 765
12366 Phe Phe Asp Gly Ala Trp His Thr Val Leu Ile Gly Thr Leu Gly Ala
12367         770                 775                 780
12368 Gly Gly Arg Gly Leu Phe Ala Leu Asp Val Thr Lys Pro Asp Asp Val
12369 785                 790                 795                 800
12370 Lys Leu Leu Trp Glu Tyr Asp Ser Ser Thr Asp Ser Asp Leu Gly Tyr
12371             805                 810                 815
12372 Thr Phe Ser Lys Pro Thr Val Ala Arg Leu His Ser Gly Gln Trp Ala
12373             820                 825                 830
12374 Val Val Thr Gly Asn Gly Tyr Gly Ser Asp Asn Asp Lys Ala Ala Leu
12375             835                 840                 845
12376 Leu Leu Ile Asp Leu Lys Lys Gly Thr Leu Ile Lys Lys Leu Glu Val
12377         850                 855                 860
12378 Gln Ser Glu Arg Gly Ile Ala Asn Gly Leu Ser Thr Pro Arg Leu Ala
12379 865                 870                 875                 880
12380 Asp Asn Asn Ser Asp Gly Ile Ala Asp Tyr Ala Tyr Ala Gly Asp Leu
12381             885                 890                 895
12382 Gln Gly Asn Ile Trp Arg Phe Asp Leu Ile Gly Asn Thr Arg Asn Asp
12383             900                 905                 910
12384 Asp Pro Asp Thr Asn Thr Ser Ile Asn Pro Phe Lys Pro Gly Asp Val
12385         915                 920                 925
12386 Asp Pro Ser Ala Phe Arg Val Ser Phe Ser Gly Ala Pro Leu Phe Arg
12387         930                 935                 940
12388 Ala Arg Ala Asp Asn Asn Thr Arg Gln Pro Ile Thr Ala Pro Pro Thr
12389 945                 950                 955                 960
12390 Leu Val Arg His Pro Ser Arg Lys Gly Tyr Ile Val Ile Val Gly Thr
12391             965                 970                 975
12392 Gly Lys Tyr Phe Glu Asp Asp Asp Ala Gln Ala Asp Thr Ser Arg Ala
12393             980                 985                 990
12394 Met Thr Leu Tyr Gly Ile Trp Asp Arg Gln Thr Lys Gly Glu Ser Ala
12395             995                 1000                1005
12396 Asn Ser Thr Pro Thr Ile Asp Arg Asn Ala Leu Thr Ala Gln Thr Met
12397         1010                1015                1020
12398 Thr Thr Glu Ala Asn Ser Thr Phe Gly Ser Val Asn Arg Asn Ile Arg
```

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\03142002\I975719.raw

```
E--> 12399 1025                1030                1035              (104) -Should
     12400 Leu Ile Ser Gln Asn Pro Val Lys Trp Tyr Lys Asp Gly Ala Thr Gly   be
     12401               1045                1050                1055       1040
     12402 Thr Ala Asn Ser Asp Val Ala Ser Tyr Gly Trp Arg Leu Asn Leu Glu
     12403               1060                1065                1070
     12404 Val Asn Ser Ser Lys Lys Gly Glu Met Met Ile Glu Asp Met Phe Ala
     12405           1075                1080                1085
     12406 Ala Gly Gln Val Leu Leu Leu Gln Thr Leu Thr Pro Asn Asp Asp Pro
     12407       1090                1095                1100
     12408 Cys Asp Ser Gly Ser Thr Ser Trp Thr Tyr Gly Leu Asn Pro Tyr Thr
E--> 12409 1105                1110                1115              (112) Should be
     12410 Gly Gly Arg Thr Ser Phe Thr Val Phe Asp Leu Lys Arg Ala Gly Ile   1120
     12411               1125                1130                1135
     12412 Val Asp Ser Gly Ser Asp Tyr Asn Gly Ser Val Val Ser Ala Phe Gln
     12413           1140                1145                1150
     12414 Gln Asp Gly Leu Gly Gly Leu Ala Ile Thr Gln Asn Glu Gln Arg Gln
     12415       1155                1160                1165
     12416 Ser Glu Ala Cys Thr Gly Asp Glu Cys Ile Ile Phe Asn Pro Ser Asp
     12417       1170                1175                1180
     12418 Lys Ser Asn Gly Arg Gln Thr Trp Arg Val Val Glu Glu Lys
     12419 1185                1190                1195
```

VERIFICATION SUMMARY   DATE: 03/14/2002
PATENT APPLICATION: **US/09/975,719**   TIME: 12:17:03

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\03142002\I975719.raw**

```
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1180 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:2979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:3037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:3090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:4325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121
L:4326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121
L:4340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122
L:4341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122
L:4342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122
L:4344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122
L:4413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128
L:4836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:4837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:4838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:12399 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:405
M:332 Repeated in SeqNo=405
```